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RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/053,758

TIME: 15:47:22

Input Set : N:\CrF3\RULE60\10053758.raw

Output Set: N:\CRF3\02062002\J053758.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Cech, Thomas R.

6 Lingner, Joachim

7 Nakamura, Toru

8 Chapman, Karen B.

9 Morin, Gregg B.

10 Harley, Calvin

11 Andrews, William H.

13 (ii) TITLE OF INVENTION: Novel Telomerase

15 (iii) NUMBER OF SEQUENCES: 225

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

19 (B) STREET: Two Embarcadero Center, 8th Floor

20 (C) CITY: San Francisco

21 (D) STATE: California

22 (E) COUNTRY: United States of America

23 (F) ZIP: 94111

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/10/053,758

C--> 33 (B) FILING DATE: 18-Jan-2002

59 (C) CLASSIFICATION: 536

56 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/854,050

38 (B) FILING DATE: 09-MAY-1997

42 (A) APPLICATION NUMBER: US 08/851,843

43 (B) FILING DATE: 06-MAY-1997

47 (A) APPLICATION NUMBER: US 08/846,017

48 (B) FILING DATE: 25-APR-1997

52 (A) APPLICATION NUMBER: US 08/844,419

53 (B) FILING DATE: 18-APR-1997

57 (A) APPLICATION NUMBER: US 08/724,643

58 (B) FILING DATE: 01-OCT-1996

61 (viii) ATTORNEY/AGENT INFORMATION:

62 (A) NAME: Apple, Randolph T.

63 (B) REGISTRATION NUMBER: 36,429

64 (C) REFERENCE/DOCKET NUMBER: 015389-002930US

66 (ix) TELECOMMUNICATION INFORMATION:

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67      (A) TELEPHONE: (415) 576-0200
68      (B) TELEFAX: (415) 576-0300
70 (2) INFORMATION FOR SEQ ID NO: 1:
72      (i) SEQUENCE CHARACTERISTICS:
73          (A) LENGTH: 3279 base pairs
74          (B) TYPE: nucleic acid
75          (C) STRANDEDNESS: single
76          (D) TOPOLOGY: linear
78      (ii) MOLECULE TYPE: other nucleic acid
79          (A) DESCRIPTION: /desc = "DNA"
81      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
83 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA      60
85 TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA      120
87 TCAAGCTGAT AATCATGGCA TTCCTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAAGC      180
89 TAAAACGTTG TACTCTTGGG TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA      240
91 TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG      300
93 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT      360
95 AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA      420
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103 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTGAA      660
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107 ATGTTGATCA ACCTGCAAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT      780
109 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT      840
111 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT      900
113 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA      960
115 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT      1020
117 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAATTTGGC GGGAACGGAA      1080
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121 GCTGTTTATG TACACAACATG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA      1200
123 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT      1260
125 TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC AAAAATTAT TGCTTGAGAA      1320
127 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA      1380
129 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT      1440
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135 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT      1620
137 TGGATTTGCA CCTGGAAGAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT      1680
139 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAATTAAT CTACAAATAC      1740
141 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC      1800
143 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTTG      1860
145 CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA ACTATGGATA TCGAAAAGTG      1920
147 ATATGATAGT GTAAACAGAG AAAAATATC AACATTCTTA AAAACTACTA AATTACTTTC      1980
149 TTCAGATTTT TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA      2040
151 TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT      2100
153 TGCAGTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA      2160
155 CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA      2220
157 TAACTTACTT CAACCAGTCA TTAATATTG CCAATATAAT TACATTAAT TTAATGGGAA      2280

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159 GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTGATC 2340
161 ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA 2400
163 CCTTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC 2460
165 AACTCAAGAG AATAATGCAG TATTGTTTTAT TGAGAAACTT ATAAACGTAA GTCGTGAAAA 2520
167 TGGATTTTAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAAGTC CAAGCAAATT 2580
169 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG 2640
171 GATTGGCATC TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT 2700
173 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT 2760
175 CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT 2820
177 TACAACCGAA GACTTTGCGA ATAAAACCTCT CAACAAGTTA TTTATATCAG GCGGTTACAA 2880
179 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAAGTAG CTATGAGCAG 2940
181 TATGATCGAC TTAGAGGTAT CTAATAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA 3000
183 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAAAGGAG CATTATCCAG ACTTTTTCCT 3060
185 TAGCACACTG AAGCACTTTA TTGAAATTTT CAGCACAAAA AAGTACATTT TCAACAGAGT 3120
187 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT 3180
189 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGT 3240
191 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG 3279

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193 (2) INFORMATION FOR SEQ ID NO: 2:

195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 1031 amino acids

197 (B) TYPE: amino acid

198 (C) STRANDEDNESS: Not Relevant

W--> 199 (D) TOPOLOGY: Not Relevant

201 (ii) MOLECULE TYPE: protein

203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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205 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
206 1 5 10 15
208 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
209 20 25 30
211 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
212 35 40 45
214 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
215 50 55 60
217 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
218 65 70 75 80
220 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
221 85 90 95
223 Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
224 100 105 110
226 Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
227 115 120 125
229 Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
230 130 135 140
232 Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
233 145 150 155 160
235 Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
236 165 170 175
238 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
239 180 185 190

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241	Asp	Lys	Lys	Gln	Lys	Gly	Gly	Ala	Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys
242			195					200					205			
244	Cys	Ser	Thr	Cys	Lys	Tyr	Asn	Val	Lys	Asn	Glu	Lys	Asp	His	Phe	Leu
245			210				215					220				
247	Asn	Asn	Ile	Asn	Val	Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg
248						230					235					240
250	Ile	Phe	Tyr	Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys
251					245					250					255	
253	His	Glu	Phe	Val	Ser	Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala
254				260					265					270		
256	Gln	Thr	Ile	Phe	Thr	Asn	Ile	Phe	Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys
257			275					280					285			
259	Leu	Lys	Asp	Lys	Val	Ile	Glu	Lys	Ile	Ala	Tyr	Met	Leu	Glu	Lys	Val
260			290				295					300				
262	Lys	Asp	Phe	Asn	Phe	Asn	Tyr	Tyr	Leu	Thr	Lys	Ser	Cys	Pro	Leu	Pro
263			305			310					315					320
265	Glu	Asn	Trp	Arg	Glu	Arg	Lys	Gln	Lys	Ile	Glu	Asn	Leu	Ile	Asn	Lys
266					325					330					335	
268	Thr	Arg	Glu	Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr
269				340					345					350		
271	Thr	Asp	Asn	Lys	Cys	Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn
272			355					360					365			
274	Ile	Leu	Pro	Lys	Asp	Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln
275			370				375					380				
277	Lys	Lys	Val	Lys	Lys	Tyr	Val	Glu	Leu	Asn	Lys	His	Glu	Leu	Ile	His
278			385			390					395					400
280	Lys	Asn	Leu	Leu	Leu	Glu	Lys	Ile	Asn	Thr	Arg	Glu	Ile	Ser	Trp	Met
281					405					410					415	
283	Gln	Val	Glu	Thr	Ser	Ala	Lys	His	Phe	Tyr	Tyr	Phe	Asp	His	Glu	Asn
284				420					425					430		
286	Ile	Tyr	Val	Leu	Trp	Lys	Leu	Leu	Arg	Trp	Ile	Phe	Glu	Asp	Leu	Val
287			435					440					445			
289	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser
290			450				455					460				
292	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met
293			465			470					475					480
295	Lys	Met	Ser	Ile	Ala	Asp	Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln
296					485					490					495	
298	Glu	Lys	Glu	Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly
299				500					505					510		
301	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr
302			515					520					525			
304	Phe	Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr
305			530				535					540				
307	Thr	Asn	Thr	Lys	Leu	Leu	Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys
308			545			550					555					560
310	Asn	Arg	Met	Phe	Lys	Asp	Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp
311					565					570				575		
313	Asp	Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val

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314				580				585				590				
316	Gly	Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr
317				595				600					605			
319	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys
320			610				615					620				
322	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg
323			625			630					635					640
325	Lys	Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met
326				645						650					655	
328	Lys	Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly
329			660						665					670		
331	Gln	Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu
332			675					680					685			
334	Asn	Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe
335			690				695					700				
337	Lys	Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn
338			705			710					715					720
340	Tyr	Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro
341				725						730					735	
343	Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr
344			740						745				750			
346	Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro
347			755					760					765			
349	Glu	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu
350			770				775					780				
352	Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu
353			785			790					795					800
355	Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
356				805						810					815	
358	Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met
359			820						825					830		
361	Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile
362			835					840					845			
364	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
365			850				855					860				
367	Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr
368			865			870					875					880
370	Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met
371				885						890					895	
373	Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe
374			900						905					910		
376	Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr
377			915					920					925			
379	Met	Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala
380			930				935					940				
382	Met	Ser	Ser	Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val
383			945			950					955					960
385	Thr	Arg	Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile
386				965						970					975	

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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L:3843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3854 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=74
L:3882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
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L:4483 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93
L:4499 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=94
L:4515 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=95
L:4531 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=96
L:4547 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=97
L:4563 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=98
L:4579 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=99
L:4722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:4820 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=102
L:4836 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=103
L:4851 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=104
L:6626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:6730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L:6733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L:6929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185
L:7302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:7748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217